SEQUENCE LISTING

```
<110> Akzo Nobel NV
<120> Structural Proteins of Fish Pancreatic Disease Virus
      and Uses Thereof
<130> I/98376US
<140> PCT/EP 99/03244
<141> 1999-05-06
<150> EP98201461.5
<151> 1998-05-08
<160> 15
<170> PatentIn Ver. 2.1
<210> 1
<211> 5179
<212> DNA
<213> Salmon pancreatic disease virus
<400> 1
gactatggac tcagcggcaa tgaacgtgga ggcttttaaa agtttcgcct gtaaggacac 60
cgacctgtgg actgagttcg cggaaaaacc agtaaggttg tcgcccggcc aaatcgaaga 120
gtatgtcttt catctacaag gggccaaggc caatgtgatg cacagcagag tcgaagccgt 180
atgccctgac ctctcggagg tggctatgga caggttcaca ctagacatga aacgcgacgt 240
caaagtgacg ccaggcacga agcacgtaga ggagagacct aaagtccaag agattcaagc 300
qqccqacccc atqqccaccq cqtacttqtq cqccatccat aqaqaqctag tccqaagqct 360
qaaqqccqtc ctgaaaccgt ctatacacgt qttgttcqat atgagctccg aggattttga 420
tgctatcqtg ggccatggga tgaagttggg tgacaaqqtg ctggaaacgg acatctcctc 480
attegacaag agecaggace aagecatgge ggttacageg etgatgetge tgagggactt 540
qqqaqtaqaa qaaqacctcc tgaccctaat tqaqqcqtct ttcqqcqaca tcacttctqc 600
ccacctgccc acaggcacca gatttcagtt tggatcgatg atgaagtctg gactttttct 660
gacgetgtte gtgaacaege tgettaacat caccataget geeegagttt taegggagea 720
gctggctgat accaggtgtg ccgcgtttat cggtgacgac aacgtaatca ccggagtagt 780
qtctqacqac atqatqqtqq ccaqqtqcqc atcctqqctq aacatqqaqq tgaaqatcat 840
ggacatggaa attggcaaca tgagtcctta tttttgtggc ggcttcctgt tactcgacac 900
ggtaacaggc actgtaagcc gagtgtcgga ccctgtaaaa cgcctgatga agatgggaaa 960
accggccctg aacgatccag aaacggacgt ggacagatgc cgcgcactgc gcgaagaagt 1020
ggaaagctgg tacagagtgg ggattcagtg gccactgcag gtggctgccg ccacacgcta 1080
tggcgtgaac cacctgccgc tggccacaat ggcgatggcc acgctcgccc aggacttgag 1140
atogtacetg ggcgcgcgag gggagtacgt atccetetac gtetaacett aatatttet 1200
gcatcatact tccaaacaat catgtttccc atgcaattca ccaactcagc ctatcgccag 1260
atggagccca tgtttgcacc gggttcccga ggacaagtac agccgtaccg gccgcgcact 1320
aagcgccgcc aggagccgca agtcggcaac gccgccatta ctgccctcgc gaaccagatg 1380
agtgcgctcc agttgcaggt agctggactt gccggccagg caagggtgga ccgccgtggg 1440
ccaagacgtg ttcagaagaa caagcagaag aagaagaact cttccaacgg agaaaaaccc 1500
aaagagaaga agaagaagca aaaacaacag gagaagaagg gaagcggtgg cgaaaaagtc 1560
aaqaaqacta qqaaccqacc cqqqaaqqaq qtaaqqatct ccqtaaaqtq tqcccqacaq 1620
agcaccttcc ccgtgtacca cgaaggtgct atatccggct acgctgtgct gattggatct 1680
cgcgtattca agccggcaca cgtgaagggt aagatcgacc accctgaact ggcagacatc 1740
aagttccagg tcgccgagga catggacctc gaagcagctg cgtacccgaa gagcatgcga 1800
gaccaagcgg ctgaaccagc gaccatgatg gacagagtgt acaactggga gtatggcact 1860
atcagagtgg aggataatgt cataatcgac gcaagcggta ggggcaagcc gggtgacagt 1920
```

```
ggcagggcca tcaccgacaa ctcgggaaag gttgttggta ttgtcctcgg aggaggaccc 1980
gatggcaggc gcacacgcct ctccgtgata ggtttcgaca agaagatgaa ggctagggag 2040
atcgcctaca gtgatgccat accttggaca cgcgctccgg ccctcctgct gctgcctatg 2100
gttattgtct gcacctacaa ttccaacacc ttcgattgct ccaaaccgtc ctgccaggac 2160
tgctgcatta ctgctgaacc agagaaggcc atgaccatgc tgaaggacaa tctgaacgac 2220
ccgaactact gggacctact cattgctgtc accacctgtg gctccgcccg gagaaagagg 2280
getgtgteta egtegeetge egeettttae gacacacaga teetegeege ceaegeaget 2340
gcctccccat acagggcgta ctgccccgat tgtgacggaa cagcgtgtat ctcgccgata 2400
gccatcgacg aggtggtgag cagtggcagc gaccacgtcc tccgcatgcg ggttggttct 2460
caatcgggag tgaccgctaa gggtggtgcg gcgggtgaga cctctctgcg atacctggga 2520
agggacggga aggttcacgc cgcagacaac acgcgactcg tggtgcgcac gactgcaaag 2580
tgcgacgtgc tgcaggccac tggccactac atcctggcca actgcccagt ggggcagagc 2640
ctaaccgttg cggccacact ggatggcacc cggcatcaat gcaccacggt tttcgaacac 2700
caagtaacgg agaagttcac cagagaacgc agcaagggcc accatctgtc cgacatgacc 2760
aagaaatgca ccagattttc cactacacca aaaaagtccg ccctctacct cgttgatgtg 2820
tatgacgete tgccgattte tgtagagatt ageacegteg taacatgcag cgacagecag 2880
tgcacagtga gggtgccacc tggtaccaca gtgaaattcg acaagaaatg caagagcgct 2940
gactoggcaa cogtoacttt caccagogac toccagaogt ttacgtgtga ggagocagto 3000
ctaacggctg ccagtatcac ccagggcaag ccacacctca gatcggcaat gttgcctagc 3060
ggaggcaagg aagtgaaagc aaggatcccg ttcccgttcc cgccggaaac cgcaacttgc 3120
agagtgagtg tagccccact gccgtcgatc acctacgagg aaagcgatgt cctgctagcc 3180
ggtaccgcaa aataccctgt gctgctaacc acacggaacc ttggtttcca tagcaacgcc 3240
acatccgaat ggatccaggg caagtacctg cgccgcatcc cggtcacgcc tcaagggatc 3300
gagctaacat ggggaaacaa cgcgccgatg cacttttggt catccgtcag gtacgcatcc 3360
ggggacgctg atgcgtaccc ctgggaactt ctggtgtacc acaccaagca ccatccagag 3420
tacgcgtggg cgtttgtagg agttgcatgc ggcctgctgg ctatcgcagc gtgcatgttt 3480
gegtgegeat geageagggt geggtactet etggtegeea acaegtteaa etegaaceea 3540
ccaccattga ccgcactgac tgcagcactg tgttgcatac caggggctcg cgcggaccaa 3600
ccctacttgg acatcattgc ctacttttta ggggtaagag ggtggtcagc cctgctggtc 3660
atcettgegt atgtacagag etgeaagage tacgaacaca eegtggtggt eecaatggat 3720
ccaagagccc cgtcgtacga agcagtgata aaccggaatg ggtatgatcc attgaagctg 3780
accatctcag tgaatttcac cgtcatctca ccaactacgg ctctggaata ttggacctgc 3840
geaggagtee ceategtega geegeeceat gtgggetget geaegteggt gteetgeece 3900
tetgacetet etaegetgea tgegtttaet ggeaaagetg teteegaegt geaetgegat 3960
gtgcacacaa acgtgtaccc cttgttgtgg ggcgcggctc actgcttctg ttccaccgag 4020
aatacacagg tcagcgctgt ggcagccacc gtttctgagt tctgtgccca ggactcagag 4080
cgtgccgaag cgttcagcgt acacagcagc tcagtcaccg ctgaggtcct ggtgacgctt 4140
ggtgaagtgg tgacggcagt ccacgtttac gtggacgggg taacatcagc caggggcact 4200
gacctcaaga tcgtggctgg accaataaca accgactact ccccattcga tcgcaaagta 4260
gtccgcatcg gcgaagaggt ctataactat gactggcctc cttacggggc tggccgacca 4320
ggcacattcg gagacattca agctaggtca accaactatg tcaaacccaa cgatctgtat 4380
ggggacatcg gaattgaagt actgcagccg actaacgacc acgtacatgt ggcttacacg 4440
tatacgacct ctgggttact gcgttggctg caggacgctc cgaaaccact cagtgtcaca 4500
geacegeacg gttgtaagat cagtgeeaat eegeteetgg eeetegattg tggggttggt 4560
geogteecca tgtecateaa catteeggae gegaagttta eeegcaaatt aaaggateeg 4620
aaaccatcgg ccctgaaatg cgtggtggac agctgcgagt acggggtgga ctacgggggc 4680
gccgccacga tcacctacga gggccacgag gccgggaagt gcgggattca ttccctgaca 4740
ccaggagtcc ccctgagaac atcggtggtt gaagtggttg ctggcgccaa taccgtcaaa 4800
acgaccttct cctcacccac gcccgaggtt gcactcgagg tagagatctg ttcggcaata 4860
gtgaagtgcg ctggtgagtg cactccaccg aaggaacatg tggtcgcaac caggcctcgc 4920
catggcagcg accetggagg ctacatetee gggceegeaa tgegetggge eggagggatt 4980
gtagggaccc tagtggtcct gttccttatc cttgccgtca tctactgcgt ggtgaagaag 5040
tgccgctcca aaagaatccg gatagtcaag agctaaattc cggtatacaa attgctcact 5100
aggageceat ecgateceae agggagtagg atgagteate tattggtttt aaaattttea 5160
atacaaaaaa aaaaaaaa
                                                                  5179
```

```
<210> 2
<211> 394
<212> PRT
<213> Salmon pancreatic disease virus
<220>
<223> NSP4 (C-terminal region)
Thr Met Asp Ser Ala Ala Met Asn Val Glu Ala Phe Lys Ser Phe Ala
Cys Lys Asp Thr Asp Leu Trp Thr Glu Phe Ala Glu Lys Pro Val Arg
Leu Ser Pro Gly Gln Ile Glu Glu Tyr Val Phe His Leu Gln Gly Ala
Lvs Ala Asn Val Met His Ser Arg Val Glu Ala Val Cys Pro Asp Leu
Ser Glu Val Ala Met Asp Arg Phe Thr Leu Asp Met Lys Arg Asp Val
Lys Val Thr Pro Gly Thr Lys His Val Glu Glu Arg Pro Lys Val Gln
Glu Ile Gln Ala Ala Asp Pro Met Ala Thr Ala Tyr Leu Cys Ala Ile
            100
                                105
His Arg Glu Leu Val Arg Arg Leu Lys Ala Val Leu Lys Pro Ser Ile
                            120
His Val Leu Phe Asp Met Ser Ser Glu Asp Phe Asp Ala Ile Val Gly
                        135
                                            140
    130
His Gly Met Lys Leu Gly Asp Lys Val Leu Glu Thr Asp Ile Ser Ser
                    150
Phe Asp Lys Ser Gln Asp Gln Ala Met Ala Val Thr Ala Leu Met Leu
                                    170
Leu Arg Asp Leu Gly Val Glu Glu Asp Leu Leu Thr Leu Ile Glu Ala
Ser Phe Gly Asp Ile Thr Ser Ala His Leu Pro Thr Gly Thr Arg Phe
                            200
Gln Phe Gly Ser Met Met Lys Ser Gly Leu Phe Leu Thr Leu Phe Val
                                            220
    210
                        215
Asn Thr Leu Leu Asn Ile Thr Ile Ala Ala Arg Val Leu Arg Glu Gln
                    230
```

Leu Ala Asp Thr Arg Cys Ala Ala Phe Ile Gly Asp Asp Asn Val Ile

245

250

Thr Gly Val Val Ser Asp Asp Met Met Val Ala Arg Cys Ala Ser Trp 260 265 270

Leu Asn Met Glu Val Lys Ile Met Asp Met Glu Ile Gly Asn Met Ser · 275 280 285

Pro Tyr Phe Cys Gly Gly Phe Leu Leu Leu Asp Thr Val Thr Gly Thr 290 295 300

Val Ser Arg Val Ser Asp Pro Val Lys Arg Leu Met Lys Met Gly Lys 305 310 315 320

Pro Ala Leu Asn Asp Pro Glu Thr Asp Val Asp Arg Cys Arg Ala Leu 325 330 335

Arg Glu Glu Val Glu Ser Trp Tyr Arg Val Gly Ile Gln Trp Pro Leu 340 345 350

Gln Val Ala Ala Ala Thr Arg Tyr Gly Val Asn His Leu Pro Leu Ala 355 360 365

Thr Met Ala Met Ala Thr Leu Ala Gln Asp Leu Arg Ser Tyr Leu Gly 370 375 380

Ala Arg Gly Glu Tyr Val Ser Leu Tyr Val 385 390

<210> 3

<211> 1359

<212> PRT

<213> Salmon pancreatic disease virus

<220>

<223> p130

<400> 3

Met Pro Arg Thr Ala Arg Arg Ser Gly Lys Leu Val Gln Ser Gly Asp 1 5 10 15

Ser Val Ala Thr Ala Gly Gly Cys Arg His Thr Leu Trp Arg Glu Pro 20 25 30

Pro Ala Ala Gly His Asn Gly Asp Gly His Ala Arg Pro Gly Leu Glu 35 40 45

Ile Val Pro Gly Arg Ala Arg Gly Val Arg Ile Pro Leu Arg Leu Thr
50 55 60

Leu Ile Phe Ser Ala Ser Tyr Phe Gln Thr Ile Met Phe Pro Met Gln 65 70 75 80

Phe Thr Asn Ser Ala Tyr Arg Gln Met Glu Pro Met Phe Ala Pro Gly
85 90 95

Ser Arg Gly Gln Val Gln Pro Tyr Arg Pro Arg Thr Lys Arg Arg Gln

Glu Pro Gln Val Gly Asn Ala Ala Ile Thr Ala Leu Ala Asn Gln Met 120 Ser Ala Leu Gln Leu Gln Val Ala Gly Leu Ala Gly Gln Ala Arg Val 135 Asp Arg Arg Gly Pro Arg Arg Val Gln Lys Asn Lys Gln Lys Lys 155 Asn Ser Ser Asn Gly Glu Lys Pro Lys Glu Lys Lys Lys Gln Lys 170 Gln Gln Glu Lys Lys Gly Ser Gly Glu Lys Val Lys Lys Thr Arg 185 Asn Arg Pro Gly Lys Glu Val Arg Ile Ser Val Lys Cys Ala Arg Gln 200 Ser Thr Phe Pro Val Tyr His Glu Gly Ala Ile Ser Gly Tyr Ala Val 210 215 Leu Ile Gly Ser Arg Val Phe Lys Pro Ala His Val Lys Gly Lys Ile 230 Asp His Pro Glu Leu Ala Asp Ile Lys Phe Gln Val Ala Glu Asp Met 245 250 Asp Leu Glu Ala Ala Ala Tyr Pro Lys Ser Met Arg Asp Gln Ala Ala 260 Glu Pro Ala Thr Met Met Asp Arg Val Tyr Asn Trp Glu Tyr Gly Thr Ile Arg Val Glu Asp Asn Val Ile Ile Asp Ala Ser Gly Arg Gly Lys 290 295 Pro Gly Asp Ser Gly Arg Ala Ile Thr Asp Asn Ser Gly Lys Val Val 310 Gly Ile Val Leu Gly Gly Gly Pro Asp Gly Arg Arg Thr Arg Leu Ser 330 Val Ile Gly Phe Asp Lys Lys Met Lys Ala Arg Glu Ile Ala Tyr Ser Asp Ala Ile Pro Trp Thr Arg Ala Pro Ala Leu Leu Leu Pro Met 360 Val Ile Val Cys Thr Tyr Asn Ser Asn Thr Phe Asp Cys Ser Lys Pro 375 380 Ser Cys Gln Asp Cys Cys Ile Thr Ala Glu Pro Glu Lys Ala Met Thr 385 395 Met Leu Lys Asp Asn Leu Asn Asp Pro Asn Tyr Trp Asp Leu Leu Ile Ala Val Thr Thr Cys Gly Ser Ala Arg Arg Lys Arg Ala Val Ser Thr 425 Ser Pro Ala Ala Phe Tyr Asp Thr Gln Ile Leu Ala Ala His Ala Ala 440 Ala Ser Pro Tyr Arg Ala Tyr Cys Pro Asp Cys Asp Gly Thr Ala Cys 455 Ile Ser Pro Ile Ala Ile Asp Glu Val Val Ser Ser Gly Ser Asp His 470 475 Val Leu Arg Met Arg Val Gly Ser Gln Ser Gly Val Thr Ala Lys Gly 490 Gly Ala Ala Gly Glu Thr Ser Leu Arg Tyr Leu Gly Arg Asp Gly Lys 505 Val His Ala Ala Asp Asn Thr Arg Leu Val Val Arg Thr Thr Ala Lys Cys Asp Val Leu Gln Ala Thr Gly His Tyr Ile Leu Ala Asn Cys Pro 535 Val Gly Gln Ser Leu Thr Val Ala Ala Thr Leu Asp Gly Thr Arg His 550 555 Gln Cys Thr Thr Val Phe Glu His Gln Val Thr Glu Lys Phe Thr Arg 570 565 Glu Arg Ser Lys Gly His His Leu Ser Asp Met Thr Lys Lys Cys Thr 585 Arg Phe Ser Thr Thr Pro Lys Lys Ser Ala Leu Tyr Leu Val Asp Val 600 . 595 Tyr Asp Ala Leu Pro Ile Ser Val Glu Ile Ser Thr Val Val Thr Cys Ser Asp Ser Gln Cys Thr Val Arg Val Pro Pro Gly Thr Thr Val Lys Phe Asp Lys Lys Cys Lys Ser Ala Asp Ser Ala Thr Val Thr Phe Thr Ser Asp Ser Gln Thr Phe Thr Cys Glu Glu Pro Val Leu Thr Ala Ala 665 Ser Ile Thr Gln Gly Lys Pro His Leu Arg Ser Ala Met Leu Pro Ser 675 680 685 Gly Gly Lys Glu Val Lys Ala Arg Ile Pro Phe Pro Phe Pro Glu Thr Ala Thr Cys Arg Val Ser Val Ala Pro Leu Pro Ser Ile Thr Tyr Glu Glu Ser Asp Val Leu Leu Ala Gly Thr Ala Lys Tyr Pro Val Leu 735

Leu Thr Thr Arg Asn Leu Gly Phe His Ser Asn Ala Thr Ser Glu Trp 750

705

Ile Gln Gly Lys Tyr Leu Arg Arg Ile Pro Val Thr Pro Gln Gly Ile 755 760 765

Glu Leu Thr Trp Gly Asn Asn Ala Pro Met His Phe Trp Ser Ser Val 770 775 780

Arg Tyr Ala Ser Gly Asp Ala Asp Ala Tyr Pro Trp Glu Leu Leu Val 785 790 795 800

Tyr His Thr Lys His His Pro Glu Tyr Ala Trp Ala Phe Val Gly Val 805 810 815

Ala Cys Gly Leu Leu Ala Ile Ala Ala Cys Met Phe Ala Cys Ala Cys 820 825 830

Ser Arg Val Arg Tyr Ser Leu Val Ala Asn Thr Phe Asn Ser Asn Pro 835 840 845

Pro Pro Leu Thr Ala Leu Thr Ala Ala Leu Cys Cys Ile Pro Gly Ala 850 855 860

Arg Ala Asp Gln Pro Tyr Leu Asp Ile Ile Ala Tyr Phe Leu Gly Val 865 870 875 880

Arg Gly Trp Ser Ala Leu Leu Val Ile Leu Ala Tyr Val Gln Ser Cys 885 890 895

Lys Ser Tyr Glu His Thr Val Val Pro Met Asp Pro Arg Ala Pro 900 905 910

Ser Tyr Glu Ala Val Ile Asn Arg Asn Gly Tyr Asp Pro Leu Lys Leu 915 920 925

Thr Ile Ser Val Asn Phe Thr Val Ile Ser Pro Thr Thr Ala Leu Glu 930 935 940

Tyr Trp Thr Cys Ala Gly Val Pro Ile Val Glu Pro Pro His Val Gly 945 950 955 960

Cys Cys Thr Ser Val Ser Cys Pro Ser Asp Leu Ser Thr Leu His Ala 965 970 975

Phe Thr Gly Lys Ala Val Ser Asp Val His Cys Asp Val His Thr Asn 980 985 990

Val Tyr Pro Leu Leu Trp Gly Ala Ala His Cys Phe Cys Ser Thr Glu 995 1000 1005

Asn Thr Gln Val Ser Ala Val Ala Ala Thr Val Ser Glu Phe Cys Ala

- Gln Asp Ser Glu Arg Ala Glu Ala Phe Ser Val His Ser Ser Ser Val 1025 1030 1035 1040
- Thr Ala Glu Val Leu Val Thr Leu Gly Glu Val Val Thr Ala Val His 1045 1050 1055
- Val Tyr Val Asp Gly Val Thr Ser Ala Arg Gly Thr Asp Leu Lys Ile 1060 > 1065 1070
- Val Ala Gly Pro Ile Thr Thr Asp Tyr Ser Pro Phe Asp Arg Lys Val 1075 1080 1085
- Val Arg Ile Gly Glu Val Tyr Asn Tyr Asp Trp Pro Pro Tyr Gly 1090 1095 1100
- Ala Gly Arg Pro Gly Thr Phe Gly Asp Ile Gln Ala Arg Ser Thr Asn 1105 1110 1115 1120
- Tyr Val Lys Pro Asn Asp Leu Tyr Gly Asp Ile Gly Ile Glu Val Leu 1125 1130 1135
- Gln Pro Thr Asn Asp His Val His Val Ala Tyr Thr Tyr Thr Thr Ser 1140 1145 1150

....

- Gly Leu Leu Arg Trp Leu Gln Asp Ala Pro Lys Pro Leu Ser Val Thr 1155 1160 1165
- Ala Pro His Gly Cys Lys Ile Ser Ala Asn Pro Leu Leu Ala Leu Asp 1170 1175 1180
- Cys Gly Val Gly Ala Val Pro Met Ser Ile Asn Ile Pro Asp Ala Lys
 1185 1190 1195 1200
- Phe Thr Arg Lys Leu Lys Asp Pro Lys Pro Ser Ala Leu Lys Cys Val 1205 1210 1215
- Val Asp Ser Cys Glu Tyr Gly Val Asp Tyr Gly Gly Ala Ala Thr Ile 1220 1225 1230
- Thr Tyr Glu Gly His Glu Ala Gly Lys Cys Gly Ile His Ser Leu Thr 1235 1240 1245
- Pro Gly Val Pro Leu Arg Thr Ser Val Val Glu Val Val Ala Gly Ala 1250 1255 1260
- Asn Thr Val Lys Thr Thr Phe Ser Ser Pro Thr Pro Glu Val Ala Leu 1265 1270 1275 1280
- Glu Val Glu Ile Cys Ser Ala Ile Val Lys Cys Ala Gly Glu Cys Thr 1285 1290 1295
- Pro Pro Lys Glu His Val Val Ala Thr Arg Pro Arg His Gly Ser Asp 1300 1305 1310
- Pro Gly Gly Tyr Ile Ser Gly Pro Ala Met Arg Trp Ala Gly Gly Ile

1315 1320 1325

Val Gly Thr Leu Val Val Leu Phe Leu Ile Leu Ala Val Ile Tyr Cys 1330 1335 1340

Val Val Lys Lys Cys Arg Ser Lys Arg Ile Arg Ile Val Lys Ser 1345 1350 1355

<210> 4

<211> 282

<212> PRT

<213> Salmon pancreatic disease virus

<220>

<223> capsid

<400> 4

Met Phe Pro Met Gln Phe Thr Asn Ser Ala Tyr Arg Gln Met Glu Pro

1 5 10 15

Met Phe Ala Pro Gly Ser Arg Gly Gln Val Gln Pro Tyr Arg Pro Arg
20 25 30

Thr Lys Arg Arg Gln Glu Pro Gln Val Gly Asn Ala Ala Ile Thr Ala 35 40 45

Leu Ala Asn Gln Met Ser Ala Leu Gln Leu Gln Val Ala Gly Leu Ala 50 55 60

Gly Gln Ala Arg Val Asp Arg Arg Gly Pro Arg Arg Val Gln Lys Asn
65 70 75 80

Lys Gln Lys Lys Lys Asn Ser Ser Asn Gly Glu Lys Pro Lys Glu Lys
85 90 95

Lys Lys Gln Lys Gln Gln Glu Lys Lys Gly Ser Gly Glu Lys
100 105 110

Val Lys Lys Thr Arg Asn Arg Pro Gly Lys Glu Val Arg Ile Ser Val 115 120 125

Lys Cys Ala Arg Gln Ser Thr Phe Pro Val Tyr His Glu Gly Ala Ile 130 135 140

Ser Gly Tyr Ala Val Leu Ile Gly Ser Arg Val Phe Lys Pro Ala His 145 150 155 160

Val Lys Gly Lys Ile Asp His Pro Glu Leu Ala Asp Ile Lys Phe Gln 165 170 175

Val Ala Glu Asp Met Asp Leu Glu Ala Ala Ala Tyr Pro Lys Ser Met 180 185 190

Arg Asp Gln Ala Ala Glu Pro Ala Thr Met Met Asp Arg Val Tyr Asn 195 200 205

```
Trp Glu Tyr Gly Thr Ile Arg Val Glu Asp Asn Val Ile Ile Asp Ala
                        215
                                            220
Ser Gly Arg Gly Lys Pro Gly Asp Ser Gly Arg Ala Ile Thr Asp Asn
                    230
                                        235
Ser Gly Lys Val Val Gly Ile Val Leu Gly Gly Gly Pro Asp Gly Arg
                245
Arg Thr Arg Leu Ser Val Ile Gly Phe Asp Lys Lys Met Lys Ala Arg
                                265
Glu Ile Ala Tyr Ser Asp Ala Ile Pro Trp
<210> 5
<211> 71
<212> PRT
<213> Salmon pancreatic disease virus
<220>
<223> E3
<400> 5
Thr Arg Ala Pro Ala Leu Leu Leu Pro Met Val Ile Val Cys Thr
                                    10
Tyr Asn Ser Asn Thr Phe Asp Cys Ser Lys Pro Ser Cys Gln Asp Cys
Cys Ile Thr Ala Glu Pro Glu Lys Ala Met Thr Met Leu Lys Asp Asn
Leu Asn Asp Pro Asn Tyr Trp Asp Leu Leu Ile Ala Val Thr Thr Cys.
Gly Ser Ala Arg Arg Lys Arg
<210> 6
<211> 438
<212> PRT
<213> Salmon pancreatic disease virus
<220>
<223> E2
<400> 6
Ala Val Ser Thr Ser Pro Ala Ala Phe Tyr Asp Thr Gln Ile Leu Ala
```

Ala His Ala Ala Ser Pro Tyr Arg Ala Tyr Cys Pro Asp Cys Asp

20 25 30

Gly Thr Ala Cys Ile Ser Pro Ile Ala Ile Asp Glu Val Val Ser Ser 35 40 45 .

Gly Ser Asp His Val Leu Arg Met Arg Val Gly Ser Gln Ser Gly Val 50 55 60

Thr Ala Lys Gly Gly Ala Ala Gly Glu Thr Ser Leu Arg Tyr Leu Gly 65 70 75 80

Arg Asp Gly Lys Val His Ala Ala Asp Asn Thr Arg Leu Val Val Arg 85 90 95

Thr Thr Ala Lys Cys Asp Val Leu Gln Ala Thr Gly His Tyr Ile Leu 100 105 110

Ala Asn Cys Pro Val Gly Gln Ser Leu Thr Val Ala Ala Thr Leu Asp 115 120 125

Gly Thr Arg His Gln Cys Thr Thr Val Phe Glu His Gln Val Thr Glu 130 135 140

Lys Phe Thr Arg Glu Arg Ser Lys Gly His His Leu Ser Asp Met Thr 145 150 155 160

Lys Lys Cys Thr Arg Phe Ser Thr Thr Pro Lys Lys Ser Ala Leu Tyr 165 170 175

Leu Val Asp Val Tyr Asp Ala Leu Pro Ile Ser Val Glu Ile Ser Thr 180 185 190

Val Val Thr Cys Ser Asp Ser Gln Cys Thr Val Arg Val Pro Pro Gly
195 200 205

Thr Thr Val Lys Phe Asp Lys Lys Cys Lys Ser Ala Asp Ser Ala Thr 210 215 . 220

Val Thr Phe Thr Ser Asp Ser Gln Thr Phe Thr Cys Glu Glu Pro Val 225 230 235 240

Leu Thr Ala Ala Ser Ile Thr Gln Gĺy Lys Pro His Leu Arg Ser Ala 245 250 255

Met Leu Pro Ser Gly Gly Lys Glu Val Lys Ala Arg Ile Pro Phe Pro 260 265 270

Phe Pro Pro Glu Thr Ala Thr Cys Arg Val Ser Val Ala Pro Leu Pro 275 280 285

Ser Ile Thr Tyr Glu Glu Ser Asp Val Leu Leu Ala Gly Thr Ala Lys 290 295 300

Tyr Pro Val Leu Leu Thr Thr Arg Asn Leu Gly Phe His Ser Asn Ala 305 310 315 320

Thr Ser Glu Trp Ile Gln Gly Lys Tyr Leu Arg Arg Ile Pro Val Thr

Pro Gln Gly Ile Glu Leu Thr Trp Gly Asn Asn Ala Pro Met His Phe 340 345 350

Trp Ser Ser Val Arg Tyr Ala Ser Gly Asp Ala Asp Ala Tyr Pro Trp 355 360 365

Glu Leu Leu Val Tyr His Thr Lys His His Pro Glu Tyr Ala Trp Ala 370 > 375 380

Phe Val Gly Val Ala Cys Gly Leu Leu Ala Ile Ala Ala Cys Met Phe 385 390 395 400

Ala Cys Ala Cys Ser Arg Val Arg Tyr Ser Leu Val Ala Asn Thr Phe 405 410 415

Asn Ser Asn Pro Pro Pro Leu Thr Ala Leu Thr Ala Ala Leu Cys Cys 420 425 430

Ile Pro Gly Ala Arg Ala 435

<210> 7

<211> 32

<212> PRT

<213> Salmon pancreatic disease virus

<220>

<223> 6K

<400> 7

Asp Gln Pro Tyr Leu Asp Ile Ile Ala Tyr Phe Leu Gly Val Arg Gly
1 5 10 15

Trp Ser Ala Leu Leu Val Ile Leu Ala Tyr Val Gln Ser Cys Lys Ser 20 25 30

<210> 8

<211> 461

<212> PRT

<213> Salmon pancreatic disease virus

<220>

<223> E1

<400> 8

Tyr Glu His Thr Val Val Val Pro Met Asp Pro Arg Ala Pro Ser Tyr 1 5 10 15

Glu Ala Val Ile Asn Arg Asn Gly Tyr Asp Pro Leu Lys Leu Thr Ile 20 25 30

Ser Val Asn Phe Thr Val Ile Ser Pro Thr Thr Ala Leu Glu Tyr Trp . 35 40 45

Thr Cys Ala Gly Val Pro Ile Val Glu Pro Pro His Val Gly Cys Cys 50 55 60

Thr Ser Val Ser Cys: Pro Ser Asp Leu Ser Thr Leu His Ala Phe Thr 65 70 75 80

Gly Lys Ala Val Ser Asp Val His Cys Asp Val His Thr Asn Val Tyr 85 90 95

Pro Leu Leu Trp Gly Ala Ala His Cys Phe Cys Ser Thr Glu Asn Thr
100 105 110

Gln Val Ser Ala Val Ala Ala Thr Val Ser Glu Phe Cys Ala Gln Asp 115 120 125

Ser Glu Arg Ala Glu Ala Phe Ser Val His Ser Ser Ser Val Thr Ala 130 135 140

Glu Val Leu Val Thr Leu Gly Glu Val Val Thr Ala Val His Val Tyr 145 150 155 160

Val Asp Gly Val Thr Ser Ala Arg Gly Thr Asp Leu Lys Ile Val Ala 165 170 175

Gly Pro Ile Thr Thr Asp Tyr Ser Pro Phe Asp Arg Lys Val Val Arg 180 185 190

Ile Gly Glu Glu Val Tyr Asn Tyr Asp Trp Pro Pro Tyr Gly Ala Gly
195 200 205

Arg Pro Gly Thr Phe Gly Asp Ile Gln Ala Arg Ser Thr Asn Tyr Val 210 215 220

Lys Pro Asn Asp Leu Tyr Gly Asp Ile Gly Ile Glu Val Leu Gln Pro 225 230 235 240

Thr Asn Asp His Val His Val Ala Tyr Thr Tyr Thr Thr Ser Gly Leu
245 250 255

Leu Arg Trp Leu Gln Asp Ala Pro Lys Pro Leu Ser Val Thr Ala Pro 260 265 270

His Gly Cys Lys Ile Ser Ala Asn Pro Leu Leu Ala Leu Asp Cys Gly 275 280 285

Val Gly Ala Val Pro Met Ser Ile Asn Ile Pro Asp Ala Lys Phe Thr 290 295 300

Arg Lys Leu Lys Asp Pro Lys Pro Ser Ala Leu Lys Cys Val Val Asp 305 310 315 320

```
Ser Cys Glu Tyr Gly Val Asp Tyr Gly Gly Ala Ala Thr Ile Thr Tyr
                325
                                     330
                                                         335
Glu Gly His Glu Ala Gly Lys Cys Gly Ile His Ser Leu Thr Pro Gly
                                 345
Val Pro Leu Arg Thr Ser Val Val Glu Val Val Ala Gly Ala Asn Thr
                            360
                                                 365
Val Lys Thr Thr Phe, Ser Ser Pro Thr Pro Glu Val Ala Leu Glu Val
    370
                        375
Glu Ile Cys Ser Ala Ile Val Lys Cys Ala Gly Glu Cys Thr Pro Pro
                    390
                                         395
Lys Glu His Val Val Ala Thr Arg Pro Arg His Gly Ser Asp Pro Gly
                405
                                     410
Gly Tyr Ile Ser Gly Pro Ala Met Arg Trp Ala Gly Gly Ile Val Gly
            420
                                 425
Thr Leu Val Val Leu Phe Leu Ile Leu Ala Val Ile Tyr Cys Val Val
                            440
Lys Lys Cys Arg Ser Lys Arg Ile Arg Ile Val Lys Ser
    450
<210> 9
<211> 37
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: primer
<400> 9
tgcatgcggc cgcatgtttc ccatgcaatt caccaac
                                                                   37
<210> 10
<211> 37
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
<400> 10
tgcatgcggc cgcttgtatt gaaaatttta aaaccaa
                                                                   37
<210> 11
<211> 37
<212> DNA
```

<213> Artificial Sequence

```
<220>
<223> Description of Artificial Sequence: primer
                                                                    37
tgcatgcggc cgcatgacac gcgctccggc cctcctg
<210> 12
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
<400> 12
tgcatgcggc cgctcacgcg cgagcccctg gtatgcaaca
                                                                    40
<210> 13
<211> 37
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
                                                                    37
tgcatgcggc cgcatggctg tgtctacgtc gcctgcc
<210> 14
<211> 204
<212> DNA
<213> Salmon pancreatic disease virus
<220>
<221> CDS
<222> (1)..(204)
<223> 6K
<400> 14
gac caa ccc tac ttg gac atc att gcc tac ttg tgg acc aac agc aaa
Asp Gln Pro Tyr Leu Asp Ile Ile Ala Tyr Leu Trp Thr Asn Ser Lys
                                      10
                                                          15
gtg gcc ttc ggg cta caa ttt gcg gcg ccc gtg gcc tgt gtg ctc atc
Val Ala Phe Gly Leu Gln Phe Ala Ala Pro Val Ala Cys Val Leu Ile
             20
                                  25
att aca tac gcc ctt agg cac tgc aga ttg tgc tgc aag tct ttt tta
                                                                    144
Ile Thr Tyr Ala Leu Arg His Cys Arg Leu Cys Cys Lys Ser Phe Leu
         35
                                                                    192
qqq qta aga ggg tgg tca gcc ctg ctg gtc atc ctt gcg tat gta cag
Gly Val Arg Gly Trp Ser Ala Leu Leu Val Ile Leu Ala Tyr Val Gln
```

55

60

50

204

agc tgc aag agc Ser Cys Lys Ser 65

<210> 15

<211> 68

<212> PRT

<213> Salmon pancreatic disease virus

<400> 15

Asp Gln Pro Tyr Leu Asp Ile Ile Ala Tyr Leu Trp Thr Asn Ser Lys
1 5 10 15

Val Ala Phe Gly Leu Gln Phe Ala Ala Pro Val Ala Cys Val Leu Ile 20 25 30

Ile Thr Tyr Ala Leu Arg His Cys Arg Leu Cys Cys Lys Ser Phe Leu 35 40 45

Gly Val Arg Gly Trp Ser Ala Leu Leu Val Ile Leu Ala Tyr Val Gln
50 55 60

Ser Cys Lys Ser 65